

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, Distribution rights by IntelliGenetics, Inc. ٥.×

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

abular output not generated on: Wed Aug 20 09:44:12 1997; MasPar time 12.79 Sec 665.067 Million cell Seconds updates/sec

Description: Perfect Score: Sequence: Title: >US-08-469-637A-2 (1-401) from US08469637A.pep (1 of 2) 3030 1 MNKLLCCALVFLDISIKWTT.....QKLFLEMIGNQVQSVKISCL 401

Searched: 59021 seqs, 21210388 residues Scoring table:

РАМ 150 Gap 11

Post-processing: Minimum Listing Match first 0% 45 summaries

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.313; Variance 81.174; scale 0.595

and is derived by analysis of the total score distribution. Pred. No. is the number of results predicted by chance score greater than or equal to the score of the result to have being pr printed,

SUMMARIES

1	2013 2013 2013 2013 2013	13.4 10.0 9.7 8.9 8.9 8.6 7.7 7.3 7.3	24451 22774 22774 2445 2445 255 257 257 257	10012299	TNR2_HUMAN TNR2_MOUSE CD40_HUMAN CD40_MOUSE VT2_MYXVL TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22_VARV	TUMOR NECROSIS FACTOR TUMOR NECROSIS FACTOR CD40L RECEPTOR PRECUR CD40L RECEPTOR PRECUR TUMOR NECROSIS FACTOR LYMPHOTOXIN-BETA RECE TUMOR NECROSIS FACTOR LYMPHOTOXIN-BETA RECE PROTEIN C32 27828 HOMOL
	20222222222222222222222222222222222222	112. 90.04 8.90.00 8.97 77.12.30 80.00		1001229	TNR2_MOUSE CD40_HUMAN CD40_MOUSE VT2_MYXVL TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22_VARV	-
	30222222222222222222222222222222222222	10.0 9.7 8.9 7.1.3 6.280		1002	CD40_HUMAN CD40_MOUSE VT2_MYXVL TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22_VARV	A FA FAR
	2011 2011 2011 2011 2011 2011 2011 2011	557777888889 5		10	CD40_MOUSE VT2_MYXVL TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22_VARV	4
	2012 2013 2013 2013 2013 2013	66777778888 677786679		010	VT2_MYXVL TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22 VARV	
	2015 2015 2015 2015 2015	6677777888. 6		10	TNRC_MOUSE VT2_SFVKA TNRC_HUMAN VC22 VARV	4 A A
	2007 2007 2007	66777788. 6.0000000000000000000000000000000000		10	VT2_SFVKA TNRC_HUMAN VC22 VARV	H FA
	2233 2221 2215 2213	6.8 6.2 6.2		Q	TNRC_HUMAN	_≖ ⊅
	233 221 220 215 213 207	6.8 6.2		•	VC22 VARV	
	221 220 215 213 207	6.8 6.8		10		
	220 215 213 207	6.8 6.8 6.2		9	TNR1_MOUSE	TUMOR NECROSIS FACTOR
	215 213 207	5.2 6.8 6.2		9	TNR1_RAT	TUMOR NECROSIS FACTOR
	213	6.0 0.0		σ	NGFR_CHICK	LOW-AFFINITY NERVE GR
	207	თ თ ა დ		თ	NGFR_HUMAN	LOW-AFFINITY NERVE GR
	2	თ N		σ	NGFR_RAT	LOW-AFFINITY NERVE GR
	100			ω	FASA_BOVIN	FASL RECEPTOR PRECURS
	186	6.1		9	TNR1_PIG	TUMOR NECROSIS FACTOR
	178	5.9		N	CD30_HUMAN	CD30L RECEPTOR PRECUR
	172	5.7		φ	TNR1_HUMAN	TUMOR NECROSIS FACTOR
	159	5.2		Н	41BB_MOUSE	4-1BB LIGAND RECEPTOR
	159	5.2		N	CD27_HUMAN	CD27L RECEPTOR PRECUR
	146	4.8		7	OX40_RAT	OX40L RECEPTOR PRECUR
	144	4.8		7	OX40_MOUSE	OX401 RECEPTOR PRECUR

4 4 5 4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23
96 97	98	96	96	96	98	96	99	100	101	101	102	105	110	115	124	124	134	134	137	140	141
ω ω 2 Ν				3.2													4.4	4.4		6	4.7
3707 4092	1947			1104	494				1122 1	712			535				335	250	327	255	277
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PGBM_MOUSE DYHC_YEAST	MYSC_CAEEL	KAB7_YEAST	XCPE_XENLA	SYV_YEAST	PR31_YEAST	PHOR_SHIDY	YAQ5_SCHPO	DESP_HUMAN	YG3C_YEAST	GFA1_CANAL	LMA1_MOUSE	VWF_HUMAN	D2_DICDI	YIH9_YEAST	VA53_VACCV	VA53_VACCC	FASA_HUMAN	CD27_MOUSE	FASA_MOUSE	41BB_HUMAN	OX40_HUMAN
BASEMENT MEMBRANE-SPE DYNEIN HEAVY CHAIN, C	MYOSIN HEAVY CHAIN C	PROBABLE SERINE/THREO	CHROMOSOME ASSEMBLY P	VALYL-TRNA SYNTHETASE	PRE-MRNA SPLICING FAC	PHOSPHATE REGULON SEN	PUTATIVE TRANSLATIONA	DESMOPLAKIN I AND II	HYPOTHETICAL 128.8 KD	GLUCOSAMINE FRUCTOSE	LAMININ ALPHA-1 CHAIN	VON WILLEBRAND FACTOR	CAMP-REGULATED D2 PRO	HYPOTHETICAL 41.6 KD	PROTEIN A53.	PROTEIN A53.	FASL RECEPTOR PRECURS	CD27L RECEPTOR PRECUR	FASL RECEPTOR PRECURS	4-1BB LIGAND RECEPTOR	OX40L RECEPTOR PRECUR
7.38e-01 5.38e-01			7.38e-01	7.38e-01		7.38e-01		2.05e-01	1.48e-01	1.48e-01	1.06e-01	3.90e-02	7.01e-03	1.19e-03	4.35e-05	4.35e-05	9.35e-07	9.35e-07		8.68e-08	5.81e-08

ALIGNMENTS

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RESULT RE
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P20333;

01-FEB-1991 (REL. 17, CREATED)

01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)

01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR INDIAN PROTEIN 2) (TBPII) (P80) (TNF-R2) (P75) (CD120B).
CHARACTERIZATION.
MEDLINE; 93016040.
PENNICA D., LAM V.T., MIZE N.K.,
LIPARI M.T., GOEDDEL D.V.;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 27-31.
MEDLINE; 90110215.
ENGELMANN H., NOVICK D., WALLACH D.;
J. BIOL. CHEM. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 91045991.

KOHNO T., BREWER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,
HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.;
PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE; 90260639.

SMITH C.A., DAVIS T., ANDERSON D., SOLAM

DOWER S.K., COSMAN D., GOODWIN R.G.;

SCIENCE 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR2 OR TNFBR.
                                                                                                                                                                                                           BROCKHAUS
                                                                                                                                                                                                                                    SEQUENCE OF 22-40; 65-69; MEDLINE; 91056048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RINGOLD G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 116-461 FROM N.A., MEDLINE; 90349572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELLER R.A., SONG K.,
                                                                                                                                                                           . BIOL.
                                                                                                                                                                           CHEM. 265:20131-20138(1990).
                                                                                                                                                                                                               Ζ.
                                                                                                                                                                                                                                        SCHLAEGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONASCH M.A., FISCHER W.H., CHANG
                                                                                                                                                                                                                                                                                                            136-141; 300-306 AND 346-362.
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                                   WEBER R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L., BECKMANN M.P., JERZY R.,
                                   LEWIS
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                                   FENDLY B.M.,
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P25119;
01-MAY-1992 (REL. 2
01-MAY-1992 (REL. 2
01-OCT-1996 (REL. 2
                                                                                                                                                                                                                                                                                                              st Lou
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CONFLICT
SEQUENCE
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DISULFID
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DISULFID
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH EMBL; M33857; G339752; -.
EMBL; M35857; G339752; -.
EMBL; M55994; G339758; -.
PIR; A36077; A36007.
PIR; A36075; A36475.
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REPEAT
REPEAT
             TUMOR NECROSIS
TNFR2 OR TNFR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A23666;
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                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                  145
                                                                                                                                                                           164
                                                                                                                                                                                                                                104
                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                          31
                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL. CHEM. 267:21172-21178(1992).
FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
MUSCULUS (MOUSE).
                                                                                                                                                CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS
                                                                                                                                                                QYVKQECNRTHNRVCECKEGRY--LEI-EFC-L-KH-RSCPPGFGVVQAGTPERNTVCKR 144
                                                                                                                                                                                                                                                          YDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P19438; 1TNR
                                                                                                                                                                                                                                                                                                              Similarity 69; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00652; TNFR_NGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                   119
163
40
54
57
78
96
100
120
134
137
137
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                   AA;
                          FACTOR
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                       13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
162
201
53
67
                                                                                                                                                                                                                                                                                                                                                                   48316 MW;
                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                            Score
Pred.
26; M
                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFR-CYS 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

R -> P (IN

R -> M (IN

A -> T (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 x TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                 ? -> P (IN
? -> M (IN
. -> T (IN
0F5D0C44
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. No. 1.33e-63;
Mismatches 59;
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REF. 1).
REF. 3).
CRC32;
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                                                                                                                                                                                                                                                                                                                                     Length 461;
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                                                                                                                                                   189
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Best Local S
Matches
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MEDLINE; 91187885.
LEWIS M., TARTAGLIA L.A.
WONG G.H., CHEN E.Y., GC
PROC. NATL. ACAD. SCI. U
                                      P25942;
01-MAY-1992
01-MAY-1992
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOL. CELL. BLOW. ILLUCTOR FOR THE ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOODWIN R.G., ANDERSON D., JERZY R. COPELAND N.G., JENKINS N.A., SMITH MOL. CELL. BIOL. 11:3020-3026(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                           CD40L RECEPTOR
                                                                                              CD40_HUMAN
  HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 91246168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P19438; 1TNR.
PROSITE; PS00652; TNFR_NGFR.
                                                                                                                                                   151
                                                                                                                                                                                                                                                          38
                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                              Similarity
66; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;; TRANSMEMBRANE; (22 23 474 259 288 289 474 39 203 39 77
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                                         (REL.
                                                                                                                                                                                                                                                                                                                                                                                                        (HUMAN)
                                                                                                                                                                                                                                                                                                              Conservative
                             PRECURSOR
                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                         12.4%;
                                                                                                                                                                                                                                                                                                                                                                   50319
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GUS.A.
                                                                                                                                                                                                                                                                                                                                                                   MW;
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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                              172 sdttsstdvcrphricsi--laip--gnastdavcapes
                                                                                                                                                                                                                                                               112 tkqqnrvcaceagrycalkthsgscrqcmrlskcgpgfgvassrapngnvlckacapgtf 171
                                                                                                                                                             SNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNS
                                                                                                                                                                                                                                                                                                                         NRTHNRVCECKEGRY--LEIEF--CLKH-R-S-CPPGEGVVQAGTPERNTVCKRCPDGFF
                                                                                                                                                                                                                                                                                                        QLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQEC
                22, CREATED)
22, LAST SEQUENCE UPDATE)
29, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN;
(B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JERZY R., DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR 2
EXTRACELLULAR (POTENTIAL).
POTENTIAL,
CYTOPLASMIC (POTENTIAL).
4 X TNER-CYS.
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFR-CYS 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                             Score 375; DB 9; Le
Pred. No. 9.05e-57;
21; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DC32B2B6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A., BENNETT G.L., R
D.V.;
88:2830-2834(1991).
                                                                                         277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT; SIGNAL
                                                                                         B
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                                                                                                                                                               189
                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                              Length 474;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X50592,
PIR; S04460; S04460.
MIM; 109535; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                               01-AUG-1992 (REL. 23, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAMENKOVIC I., CLARK E.A., SEED B.;

EMBO J. 8:1403-1410(1989).

-i- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.

-i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE;
GRIMALDI J.C., TORRES R., KOZAK C.A.,
          SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 93094586.
                                                   TORRES R.M.;
SUBMITTED (S
                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 92105763.
TORRES R.M., CLARK E.A.;
J. IMMUNOL. 148:620-626(1992).
                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                            CD40_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; EUTHERIA; PRIMATES.
                                                                         STRAIN-BALB/C;
                                                                                                                                                             EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR;
                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                            156
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                                                                                                                                                                                                                                                                                                                                                                                                               cslcqpqqklvsdctefteteclpcgesefldtwnrethchqhkycdpn-lglr-vqqkg 95
                                                                                                                                                                                                                                                                                                                           safekchpwtscetkdlvvqqagtnktdvvcg
                                                                                                                                                                                                                                                                                                                                                                                          CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-L--YCSPVCKELQYVKQEC 97
                                                                                                                                                                                                                                                                                                      SSKAPCRKHTNCSVFGLLLTQKGNATHDNICS 186
                                                                                                                                                                                                                                                                                                                                                  NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 154
                                                                                                                                                                                                                                                                                                                                                                     tsetdtictceegwhctseacescvlhrscspgfgvkqiatgvsdticepcpvgffsnvs 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x60592; G29851; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00652;
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                                                                                                                                                             RODENTIA.
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                                                    (SEP-1996)
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194
216
216
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104
153
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                    TISSUE-LIVER;
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFR_NGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN;
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187
103
103
144
187
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                                                                                                                                                                       CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30619 MW;
                                                    ö
                                                    EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 303; DB 2;
Pred. No. 1.03e-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
3B284411 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR
                                                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                             289
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CHANG
                                                                                                                                                                                                                                                             A
                                                                                                                                                                       TETRAPODA; MAMMALIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 277
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CLARK E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                      (BP50) (CDW40).
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CARBOHYD
SEQUENCE
                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 9135768.

UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;

VIROLOGY 184:370-382(1991).

- FUNCTION: BINDS TO INF-LLPHA AND BETA. PROBABLY PREVENTS TNF TREACH CELULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL

ANTIVIRAL EFFECTS OF THE CYTOKINE.

-! SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

EMBL, M95121; G332310; -.

EMBL, M95121; G332310; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (REL.
01-APR-1993 (REL.
01-FEB-1994 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VT2_MYXVL
P29825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                   MYXOMA VIRUS (STRAIN LAUSANNE);
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M94127; G19252
PIR; A46476; A46476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. IMMUNOL. 149:3921-3926(1992).
-!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
-!- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOWARD M., COCKAYNE D.A.;
    DOMAIN
                                                            RECEPTOR;
                                                                                                      HSSP; P19438;
                                                                                                                       PIR; A40566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19438;
                                                                                                                                                                                                                                                                                                                                                                    EPORIPOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      slfekcypwtscedknlevlqkgtsqtnvicg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      taesdtvctckegqhctskdceacaqhtpcipgfgvmematettdtvchpcpvgffsnqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKELQYVKQEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M83312; G1553059;
M94126; G192526; CM94129; CM94129; G192526; CM94129; CM94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M94128; G192526; M94127; G192526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%;
Similarity 38.8%;
; GLYCOPROTEIN; F
1 16
17 326
27 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289
                                                                                                                       GQVZML.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25,
25,
                                                                                   TNFR_NGFR
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GLYCOPROTEIN; TRANSMEMBRANE;
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LAST ANNOTATION UPDAT
SOLUBLE RECEPTOR PREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
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JOINED.
                                                              REPEAT;
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M.
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Pred. No. 9.50e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 X TNFR-CYS.
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
AT; SIGNAL.
POTENTIAL.
PROTEIN T2.
4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNFR-CYS 4. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD40L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D8D70A2C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     POXVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
R PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                T2).
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Best Local Similarity
Matches 47; Conser
 DOMAIN
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01-0CT-1996
01-0CT-1996
01-0CT-1996
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                     IMMUNE DEVELOPMENT.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGER/TNER-TYPE CYSTE
EMBL; U20173; G881621; -.
EMBL; L38423; G600223; -.
EMBL; U30798; G1061327; -.
                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS 30:312-319(1995).
-!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 96163885. NAKAMURA T., TASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORCE W.R., WILLIAMS-ABBOTT WARE C.F.; SUBMITTED (JUN-1995) TO EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
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01-0CT-1996 (REL. 34, LAST SEQUENCE
01-0CT-1996 (REL. 34, LAST ANNOTATIC
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
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STRAIN-CVB; TISSUE-LUNG;
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34, LAST SEQUENCE UI
34, LAST ANNOTATION
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POTENTIAL
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Pred. No. 2.
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TNFR-CYS 4.
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. No. 2.38e-33;
Mismatches 58;
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MEDLINE; 87321103.
UPTON C., DELANGE A.M., M
VIROLOGY 160:20-30(1987).
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                                                                                                                                                                                                                                     HSSP; P19438;
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LEPORIPOVIRUSES
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54; Conservative
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ELOPED VIRUSES;
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MEDILIE; 91207415.

( MEDILIE; 91207415.

A MCRADDEN G., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T.,

A MCRADDEN G., GOODWIN R.G.;

L BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).

-!- FUNCTION: BINDS TO INF-ALDHA AND BETA. PROBABLY PREV.

REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTORINE.

ANTIVERAL EFFECTS OF THE CYTOKINE.

C -!- SIMILARITY: CONTAINS A LA-NGFR/INFR-TYPE CYSTEINE-RJ

R EMBL; M1743; -; NOT_ANNOTATED_CDS.

R EMBL; M1743; -; NOT_ANNOTATED_CDS.

R EMBL; M23727; E199408; -.

R EMBL; M176392. B43692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VT2_SFVKA STANDARD; PRT; 325 AA.
P25943;
P25943;
P1-MAY-1992 (REL. 22, CREATED)
P1-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
P1-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epmhdvccsrcppgefvfavcsrsqdtvcktcphnsynehwnhlstcqlcrp-cdivlgf 110
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REPEAT; SIGNAL.
POTENTIAL.
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Pred. No. 1.70e-32;
30; Mismatches 92
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POXVIRIDAE;
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01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
                     DISULFID
                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RELATED
TNFCR.
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L04270; MIM; 600979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CROWE P.D., VAN ARSDALE T.L., WALTER EHRENFELS B., BROWNING J.L., DIN W.S. SCIENCE 264:707-710(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 93252381.
BAENS M., CHAFFANET M., CASSIMAN J.J.,
GENOMICS 16:214-218(1993).
                                                                                                                                                                                               REPEAT
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SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNE DEVELOPMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNRVCECKEGRY -- L--EIE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hdrvcncstgnycllkgqngcricapqtkcpagygvs-ghtragdtlcekcpphtysdsl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sptercgtsfnyisvgfnlypvnetscttt-aghneviktkeftvtl
                                                                                                                                                                                                                                                                                                                                                                                                              P19999;
                                                                                                                                                                                                                                                                                                                                                                                            PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94225209
                                                                                                                                                                                                                                                                                                                                                        TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
                       ; iCLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             G339762; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
A
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                                                                                                                                                                                                                                                                                                                                                      GLYCOPROTEIN; REPEAT; SIGNAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 260; DB 10;
Pred. No. 1.97e-31;
31; Mismatches 77;
   BY SIMILARITY
                                                                                                                                                                                                 TNFR-CYS 3
                                                                                                                                                                                                                                TNFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         LYMPHOTOXIN-BETA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C9D2C87B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.N., WARE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŧ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 204
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SMITH C.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
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                                                                                                                                                                                                                                                                                                                                                                                                          SQUENT TO THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.6%;
Best Local Similarity 32.3%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VC22_VARV
P34015;
01-FEB-1994
01-FEB-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
SEQUENCE
TURI_MOUSE STANDARD; PRT; 454 AA P25118; 01-MAY-1992 (REL. 22, CREATED) 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-INDIA-1967 MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIOLA VIRUS.
VIRIDAE; DS-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORTHOPOXVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN C22/B28
                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                           115 -IE--FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPC
                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
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                                                                                                                                                                                                                                                                 \vdash
                                                                                                                                                                                                                                                                                            1 mksvlylyilflsciiingrdaapytppngkckdteykrhnlcclscppgtyasrlcdsk 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; D36858; D36858.
; S35987; S35987.
; S46888; S46888.
                                                                          10
                                                                                                                                             ckaghfqntsspsarcqphtrcengglveaapgtaqsdttc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epghriccsrcppgtyvsakcsrirdtvcatcaensynehwnylticqlcrpcdpv-mgl 110
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                                                                                                                                                                                            WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRY-
                                                                                                                                                                                                                  MNKLLCCALVFLD-ISIKWTTQETFPPKYLHYDE-E-TSHQLLCDKCPPGTYLKQHCTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC-LY--CSPVCKEL
                                                                                                                                                                                                                                                                                                                                    Similarity
54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00652;
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31
67
349
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435 AA;
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larity 32.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENVELOPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNFR_NGFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / ISOLATE IND3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28, CREATED)
28, LAST SEQUENCE UI
29, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                         108
38189
                                                                                                                                                                                                                                                                                                                                                                                                                                           108
66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                          ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIRUSES;
                                                                                                                                                                                                                                                                                                                                  Score 233; DB 10;
Pred. No. 9.20e-26;
26; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                       2 X INFR-CYS.
INFR-CYS 1.
TNFR-CYS 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 260; DB 9;
Pred. No. 1.97e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
203B82DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     NFR-CYS 1.
NFR-CYS 2.
50D0B435 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LEIEFCLKHRSCPPGFGV-VQAGTPERNTVCKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POXVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ON UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHORDOPOXVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                  Length 349;
                                                                                                                                                                                                                                                                                                                                    Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                            160
                                                                                                                                                           168
                                                                                                                                                                                              -EE-
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                 57
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RRAR RRAR RRAR ROCC GN DT
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C. --- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. --- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. --- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

DR EMBL; M60468; G199826; -.

DR EMBL; M59377; G202097; -.

DR EMBL; X59238; G53579; -.

DR EMBL; X59238; G53579; -.

EMBL; X57796; G54849; -.

EMBL; X57796; G54849; -.

EMBL; M76656; G202102; JOINED.

DR EMBL; M76655; G202102; JOINED.

DR EMBL; M76655; G202102; JOINED.

DR PIR; 318634; G0MST1.

DR PIR; S16677; S16677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 91187885.
LEWIS M., TARTACLIA L.A.
WONG G.H., CHEM E.Y., GC
PROC. NATL. ACAD. SCI. [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (REL. 34, LAST ANNO TUMOR NECROSIS FACTOR RECEPTOR TNFR1 OR TNFR-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VEUTHERIA; RODENTIA.
TRANSMEM
DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                             PROSITE; | PROSITE; | RECEPTOR;
                                                                                                                              CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE; 91246168.

GOODWIN R.G., ANDERSON D., JERZY R., DAVIS
COPELAND N.G., JENKINS N.A., SMITH C.A.;

MOL. CELL. BIOL. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91285014.
BARRETT K., TAYLOR-FISHWICK D.A., CO
GRAY P.W., FELDMANN M., FOXWELL B.M..
EUR. J. IMMUNOL. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                   ROTHE
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94245392.
BEBO B.F., LINVHICOM D.S.;
IMMUNOGENETICS 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92039815.
ROTHE J.G., BROCKHAUS M., GENTZ R., IMMUNOGENETICS 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A MEDLINE; 93156721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
BLUETHMANN
                                                                                                                                                                                             TNR
                                                                                                                                                                                                                                                                                                                                                        NN H., GENTZ
.65-175(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .A., LEE A., BENNETT G.L., F
GOEDDEL D.V.;
. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAST ANNOTATION UPDATE)
RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                             GLYCOPROTEIN; REPEAT; SIGNAL.
                                                    YX TNFR-CYS.
TNFR-CYS.
TNFR-CYS.
TNFR-CYS.
TNFR-CYS.
TNFR-CYS.
  DEATH
BY SIN
BY SIN
BY SIN
                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
4 x TNFR-CYS.
                                                                                                                             TUMOR NECROSIS
                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERTEBRATA; TETRAPODA; MAMMALIA;
EATH DOMAIN.

Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                 R., LESSLAUER W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPE A.P.,
                                                                                                                                         NECROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LESSLAUER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , T.,
                                                                                                                              (POTENTIAL).
                                                                                                                                        FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KISSONERGHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRANNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICE
                                                                                                                                                                                                                                                                                                                                                                  STEINMETZ M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.I.,
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RESULT TO THE PROPERTY OF THE 
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Matches
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Best Local
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REPEAT
REPEAT
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DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                  RECEPTOR;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CONFLICT
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PROSITE;
PROSITE;
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TINEL_RAT STANDARD; PRT; 461 AA.

P22934;

01-AUG-1991 (REL. 19, CREATED)

01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFR1 OR TNFR-1.
RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                             HIMMLER A., MAURER-FOGY I., KROENKE M
LANTZ M., OLSSON I., HAUPTMANN R., ST
DNA CELL BIOL. 9:705-715(1990).
-i- FUNCTION: RECEPTOR FOR TNF-ALPHA.
                                                                                                                                                                                                                                                                                                                                                       EMBL; M63122; G207362; PIR; B36555; B36555.
                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH EMBL; M63122; G207362; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 91090841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                       PS00652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RODENTIA.
                                                                                                                                                                                                                                                                                     TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
105
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50129
                                                                                                                                                                                                                                                                                                      TNFR_NGFR.
DEATH_DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
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Pred.
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POTENTIAL.
POTENTIAL.
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DEATH DOMAIN.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                     4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.
                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). 4 X THER-CYS.
                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                TUMOR NECROSIS
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4B6EEC09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRATOWA C., ADOLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; DB 9;
2.72e-23;
                                                                                                                                                                                                                                                                                     REPEAT; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC32;
                                                                                                                                                                                                                                  (POTENTIAL).
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                                                                                                                                                                                                                                                      FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                              REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT IN RESULT
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      TTTTTTTTTTWWW.RR.RCCCCCCCRA
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Best Local S
Matches 4
                PROSITE: PS00652:
PROSITE: PS50017:
RECEPTOR: NUUROGE
PHOSPHORYLATION;
SIGNAL 1
CHAIN 20
DOMAIN 240
DOMAIN 240
DOMAIN 262
DOMAIN 262
DOMAIN 263
DOMAIN 263
REPEAT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P18519;
01-NOV-1990
01-NOV-1990
01-NOV-1995
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                                                                                                                                                                                                                                                                              HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BC
DEV. BIOL. 137:287-304(1990)
-:- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN E
-:- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER
BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE OF 21-416 FROM N.A.
MEDLINE; 90152140.
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90166579.

LARGE T.H., WESKAMP G., HI
SHOOTER E.M., REICHARDT L
NEURON 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALLUS (CHICKEN)
EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGFR_CHICK
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                                                                                                                                                                                                                      PIM: N- AND O-GLYCOSYLATED .
SIMILARITY: CONTAINS > ---
; JNNOOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -chagfflsgnectpcshckknqec
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A60504; A60504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yahpknnsicctkchkgtylvsdcpspggetvcevcdkgtftasgnhvrgclscktcrke 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-QYVKQECNRTHNRVCECK--E-GRYL-EIEF-CLKHRSCPPGFGVVQAGTPERNTVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                            PS00652; TNFR_NGFR.
PS50017; DEATH_DOMAIN.
NEUROGENESIS; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
127
146
168
182
185
151
201
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(REL. 16, LAST SEQUENCE UPDATE)
(REL. 32, LAST ANNOTATION UPDATE)
      240
240
233
233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
143
158
166
179
191
195
195
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201
201
50969
                                                                                                                                   SIGNAL.
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33.8%;
      416
239
261
416
181
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               HELDER
                                                                                                                                                                                                                                A LA-NGFR/TNFR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
POTENTIAL.

NGF RECEPTOR.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

4 X THER-CYS.

THER-CYS.

THER-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 220; DB 9;
Pred. No. 4.35e-23;
22; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
POTENTIAL
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                I MEMBRANE PROTEIN.
AND IS PHOSPHORYLATED ON SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ч
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RADEKE M.J., MISKO T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416
                                                                                                                                                   GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC32;
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                                                                                                                                                                                                                                                                                                                               CAN BIND TO NGF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                  CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                               BOTHWELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                 THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 461,
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                                                                                                                                                                                                                                                                                                                                 BDNF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
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RESULTATION OF THE PROPERTY OF
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 87051725.
JOHNSON D., LANHHAN A.
BOTHWELL M., CHAO M.;
CELL 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1988 (REL. 0)
01-AUG-1988 (REL. 3)
01-NOV-1995 (REL. 3;
LOW-AFFINITY NERVE (GP80-LNGFR).
                                                                                                EMBL; M14764; G18920
PIR; A25218; GQHUN.
HSSP; P19438; 1TNR.
MIM; 162010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGFR_HUMAN
P08138;
01-AUG-1988
01-AUG-1988
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID DISULFID DISULFID DISULFID CARBOHYD CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT SEQUENCE
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REPEAT
DOMAIN
DOMAIN
DISULFID
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DISULFID
                         PROSITE; I
PROSITE; I
RECEPTOR;
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                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SEI-
-!- SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH
                                                                                                                                                                                                                                                                      -1- FUNCTION: LOW AFFINITY RECEPTOR NT-3, AND NT-4.
-1- SUBUNIT: NGF RECEPTOR CAN FORM BOND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; PRIMATES
  PHOSPHORYLATION; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
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                    PS00652; TNFR_NGFR.
PS50017; DEATH_DOMAIN.
; NEUROGENESIS; TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                           G189205;
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08, LAST SEQUENCE UPDATE)
32, LAST SEQUENCE UPDATE)
E GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
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Pred. No. 4.
27; Mismatc
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TNFF-CYS 4.
SER/THR-CYS 4.
SER/THR-CYS 4.
DEATH DOMAIN.
BY SIMILARITY
BY S
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                                                                                                                                                                                                                                                                                                  A HOMODIMER
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                         GLYCOPROTEIN;
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REF. 2).
REF. 2).
CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                                                                                                                                                  DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                            MERCER
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Best Local :
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P07174;
01-APR-1988 (REL. (
01-APR-1988 (REL. (
01-NOV-1995 (REL. 3
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CARBOHYD
SEQUENCE
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DOMAIN
REPEAT
RE
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TRANSMEM
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 87115859.
RADEKE M.J., MISKO T.P., INTURE 325:593-597(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
CHAIN
  - -
                                                           -
                                                                                                                  MEDLINE; 93077038.
METSIS M., TIMMUSK T.,
GENE 121:247-254(1992).
                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                        SEQUENCE OF 1-22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                     RATTUS NORVEGICUS (1 EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                  NGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                   (GP80-LNGFR).
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BOND FORMATION.
SUBCELLULAR LOCATION: TYPE
PTM: N- AND O-GLYCOSYLATED
                                                         FUNCTION: LOW AFFINITY REC
NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN
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                                                                                                                                                                                                                                                                                                                                                    RODENTIA.
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.larity 34.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
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32,
                                                                                                                                                                                                                                                                                                                                                                                          (RAT)
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDATE)
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                                                                                                 RECEPTOR
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Pred.
19; M
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TNFR-CYS 3.
TNFR-CYS 4.
DEATH DOMAIN.
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EXTRACELLULAR (POTENTIAL POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA;
                                                           FORM A HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
I MEMBRANE PROTEIN.
AND IS PHOSPHORYLATED ON SERINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                   HERZENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213; DB 6;
No. 1.15e-21
                                                                                                                                        SAARMA M.,
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                                                                                                    CAN
                                                                                                                                                                                                                                                                                                                                                                     TETRAPODA; MAMMALIA;
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                                                                                                                                                                                                                                                                 L.A.,
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                                                                                                    BIND
                                                             THROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                            PERSSON
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                                                                                                    NGF,
                                                             DISULFIDE
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                                                                                                                                                                                                                                                                   E.M.;
                                                                                                    BDNF,
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Best Local S
Matches 4
                                                                                                                                                                            FASA_BOVIN STANDARD; PRT; 323 AA.

P51867;

P51967;

01-OCT-1996 (REL. 34, CREATED)

01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

101-OCT-1996 (REL. 34, LAST ANNOTATION SEQUENCE OF ANNOTATION (APOPTOSIS-MEDIATING SUFFACTOR (APOPTOSIS-MEDIATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
SEQUENCE FROM N.A.

MEDLINE; 96226401.

YOO J., STONE R.T., BEATTIE C.W.
DNA CELL BIOL. 15:227-234(1996).

-!- FUNCTION: RECEPTOR FOR A CYI

CELL DEATH. FAS-MEDIATED APO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
REPEAT
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TRANSMEM
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EMBL; X61513; G56756; -.
EMBL; X61639; -; NOT_ANNOTATED_CDS.
PIR; A26431; A26431.
HSSP; P19438; ITNR.
PROSITE; P500652; TNFR_NGFR.
PROSITE; P500652; TNFR_NGFR.
PROSITE; PS00659; TNFR_NGFR.
RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APCRKHTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
43; Conser
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larity 33.3%;
Conservative
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58
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Pred.
21; M
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DEATH DOMAIN.
BY SIMILARITY
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
  CYTOKINE LIGAND KNOWN AS FASL. APOPTOSIS MAY HAVE A ROLE IN T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
7D78F258
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4 X TNFR-CYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         re 207; DB 6; Le
d. No. 1.87e-20;
Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
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                                                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                    SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 425,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                     MAMMALIA;
                                                                                                                                                                                                                                                                                                    ANTIGEN
       THE
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                              MEDIATES
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CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-CYS DOMAIN
TO CONTAINS A POTENTIAL.
CT TRANSMEM 171 188 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 189 CYTOPLASMIC (POTENTIAL).
FT REPEAT 125 163 TNFR-CYS 3.
FT DOMAIN 45 163 TNFR-CYS 3.
FT DOMAIN 222 302 TNFR-CYS 3.
FT REPEAT 125 163 TNFR-CYS 3.
FT DOMAIN 222 302 DEATH DOMAIN.
SO SEQUENCE 323 AA; 36445 MW; DASA2A59 CRC32;
SO SEQUENCE 32 AA; 36445 MW; DASA2A59 CRC32;
SO SEQUENCE 3
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